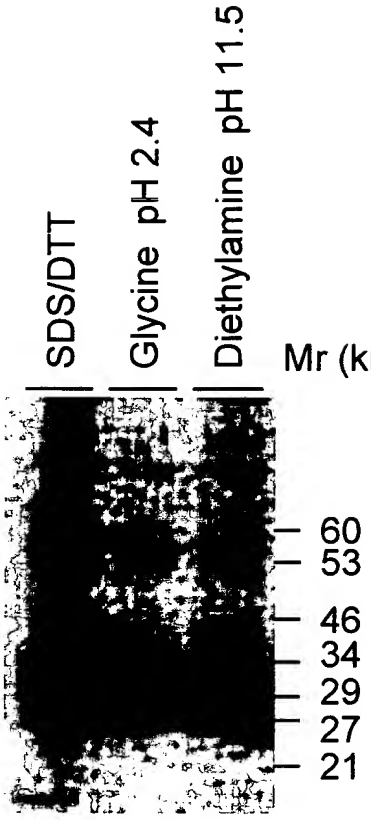

SDS/DTT
Glycine pH 2.4
Diethylamine pH 11.5
Mr (kDa)
60
53
46
34
29
27
21
reducing

FIG.1A

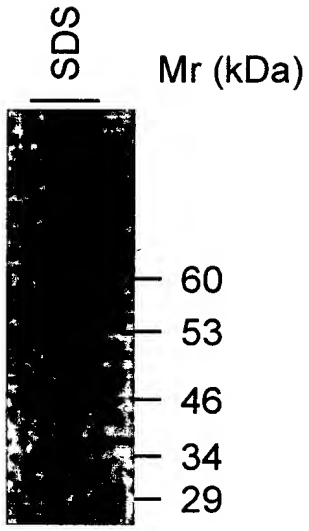

SDS
Mr (kDa)
60
53
46
34
29
non-reducing

FIG.1B

APPROVED O.G. FIG.
BY
DRAFTSMAN
CLASS SUBCLASS

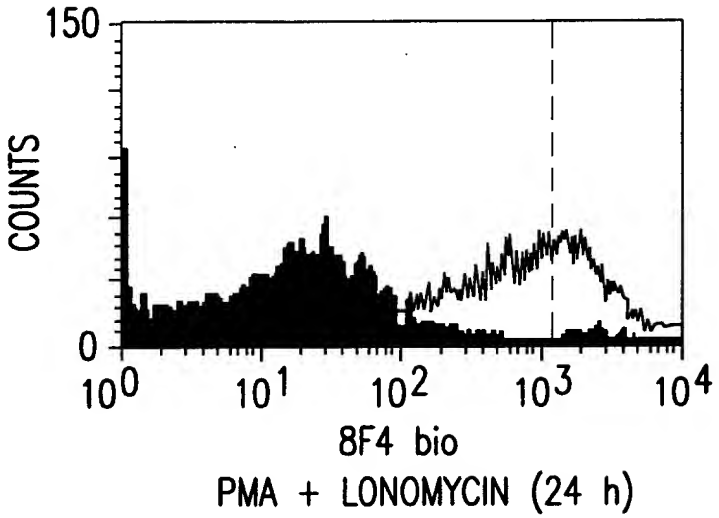


FIG.2A-1

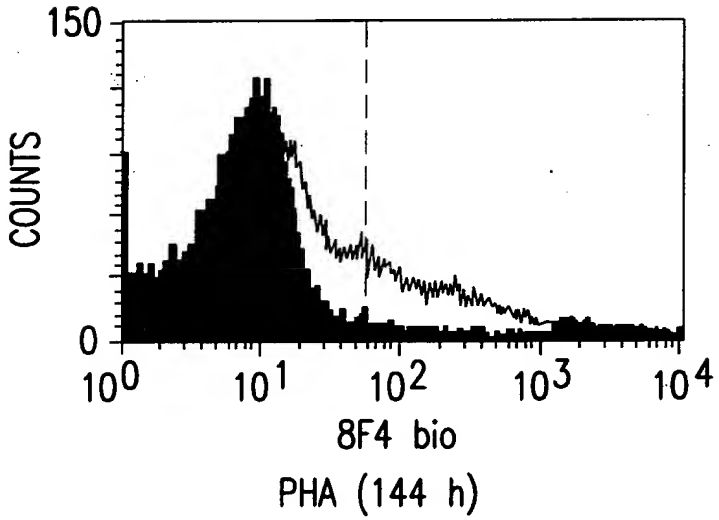


FIG.2A-2

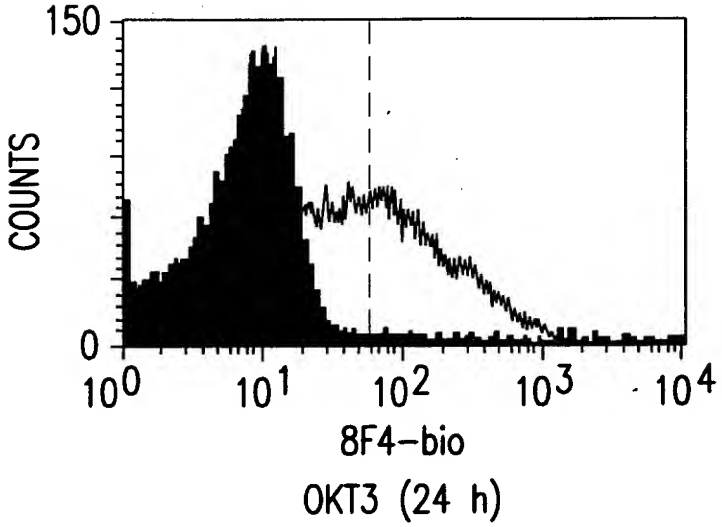


FIG.2A-3

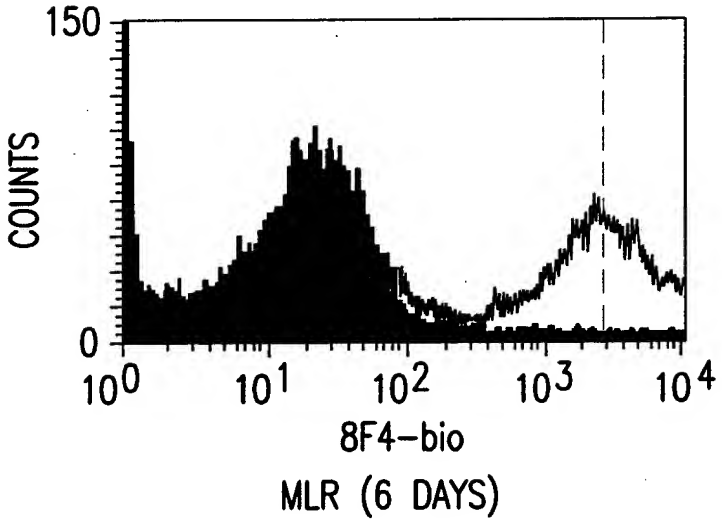


FIG.2A-4

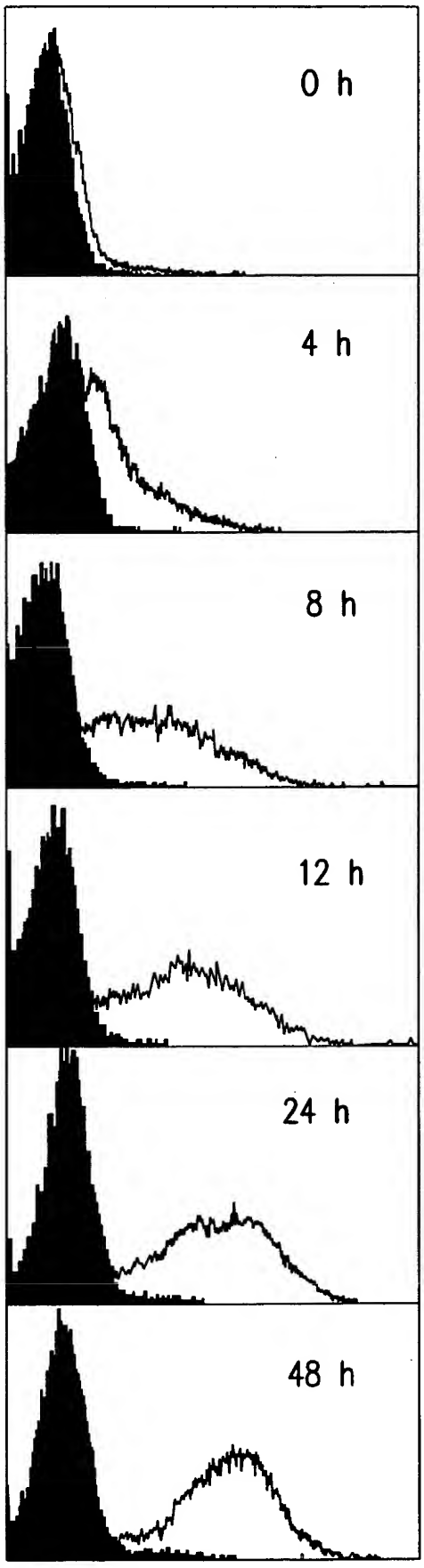


FIG.2B

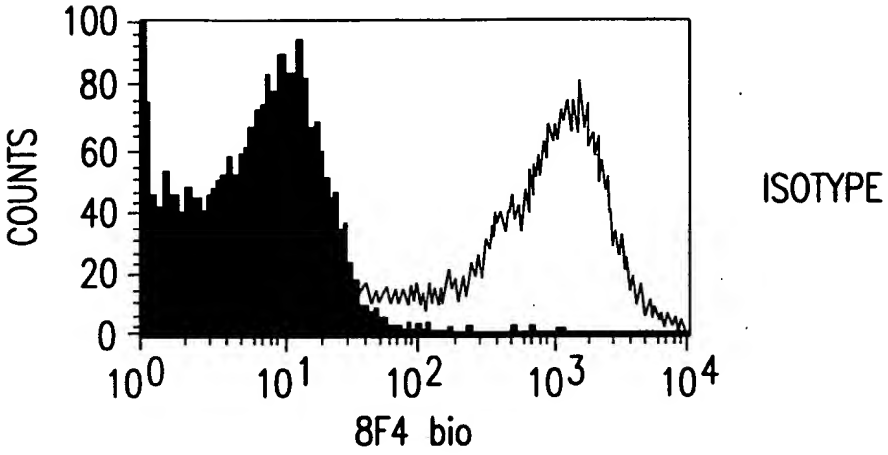


FIG.3A

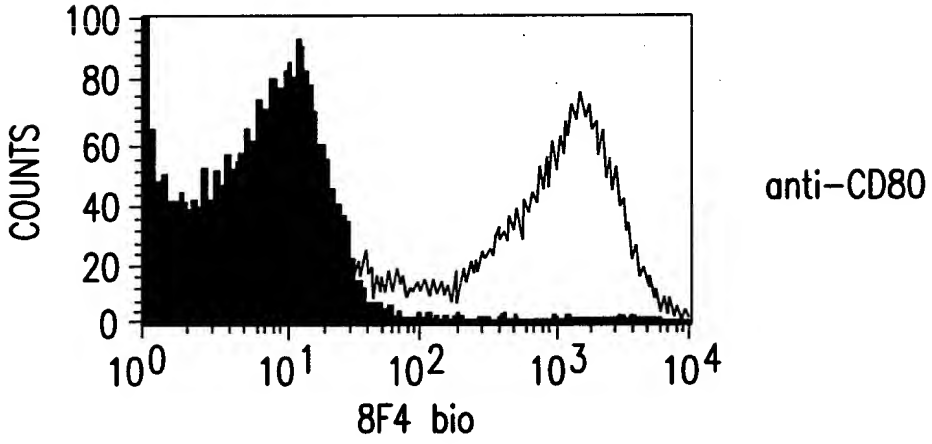


FIG.3B

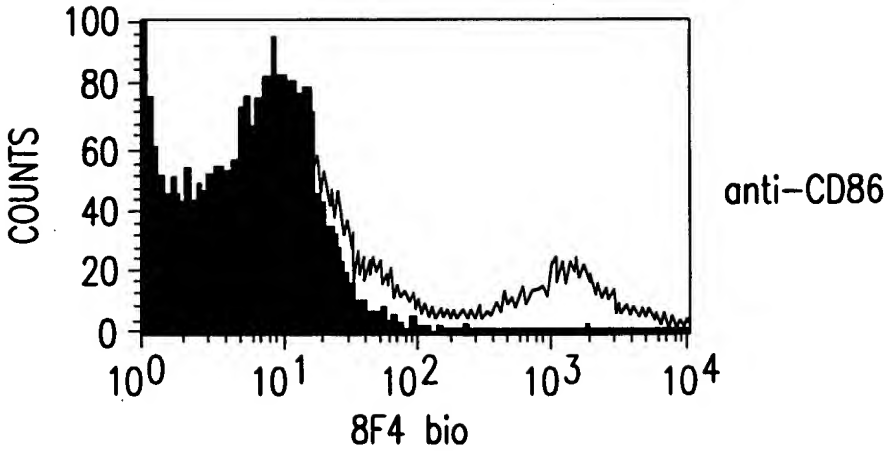
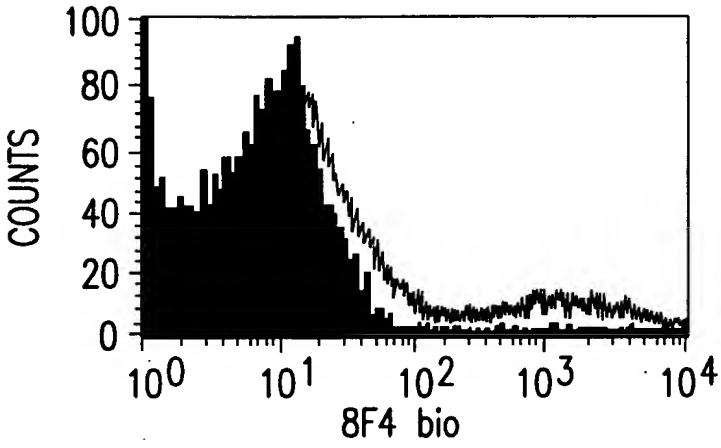
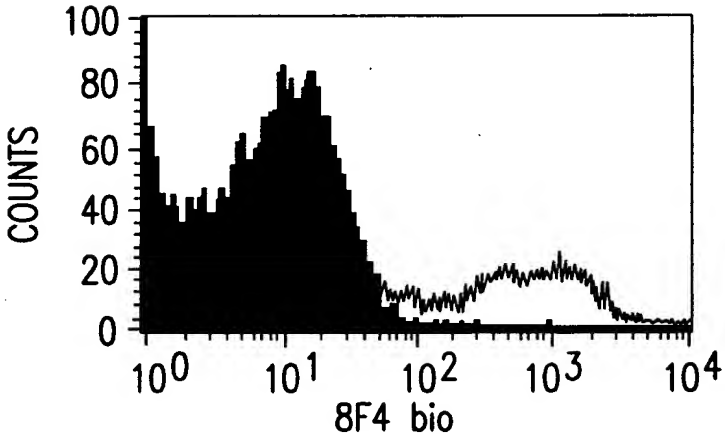


FIG.3C



anti-CD80+
anti-CD86

FIG.3D



anti-MHCII

FIG.3E

FIG.4A

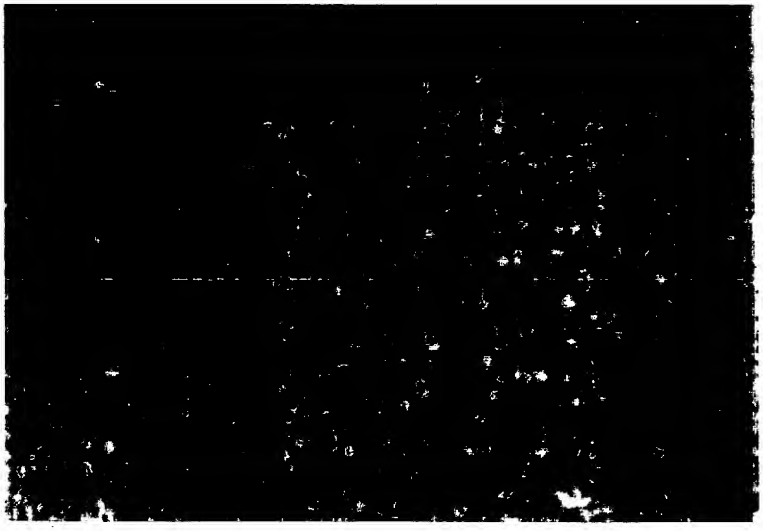


FIG.4B

TONSILLAR B CELLS

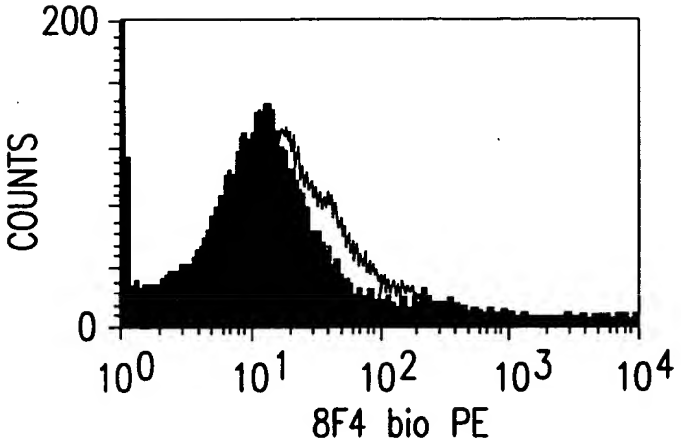


FIG.5A

TONSILLAR T CELLS

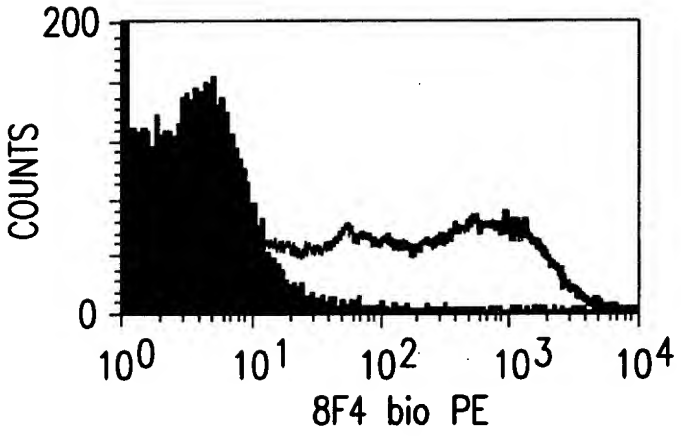


FIG.5B-1

TONSILLAR T CELLS

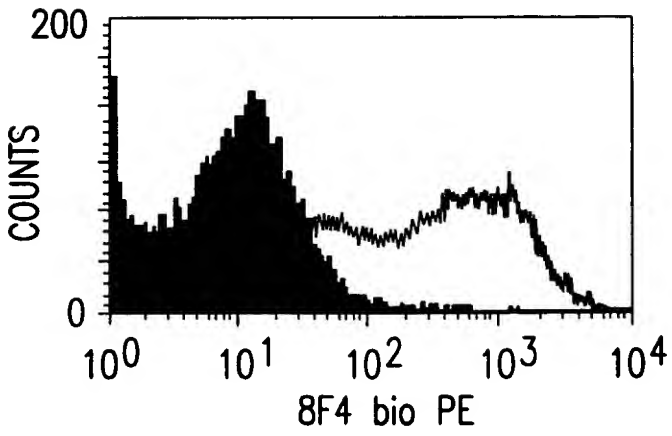


FIG.5B-2

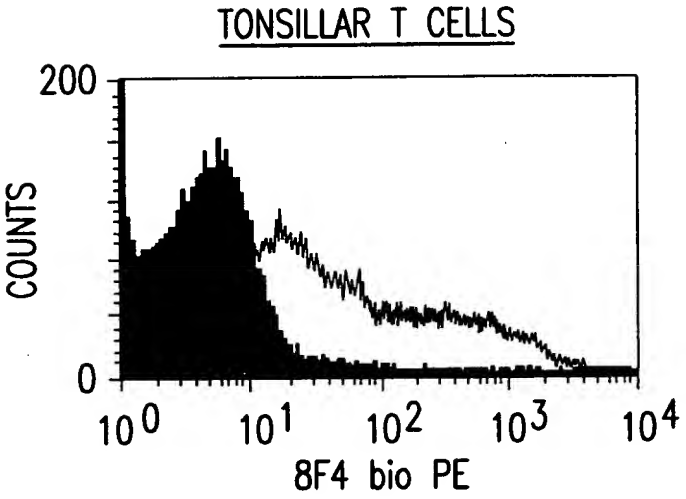


FIG.5B-3

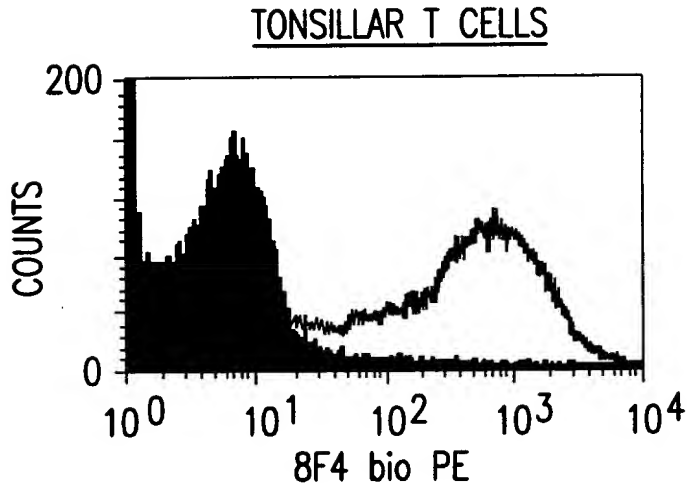


FIG.5B-4

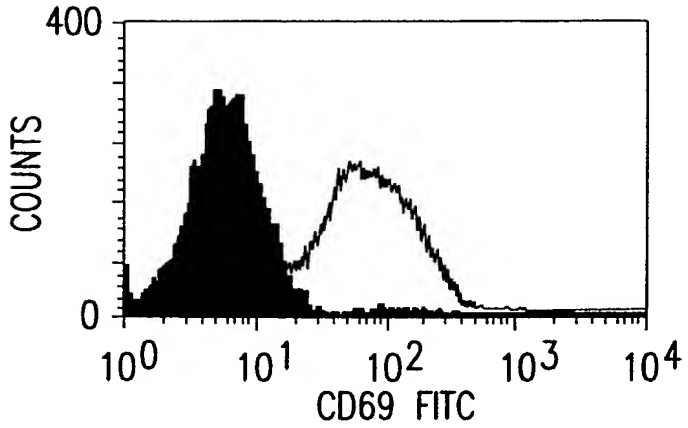

400
COUNTS
0
10^0
10^1
10^2
10^3
10^4
CD69 FITC

FIG.6A

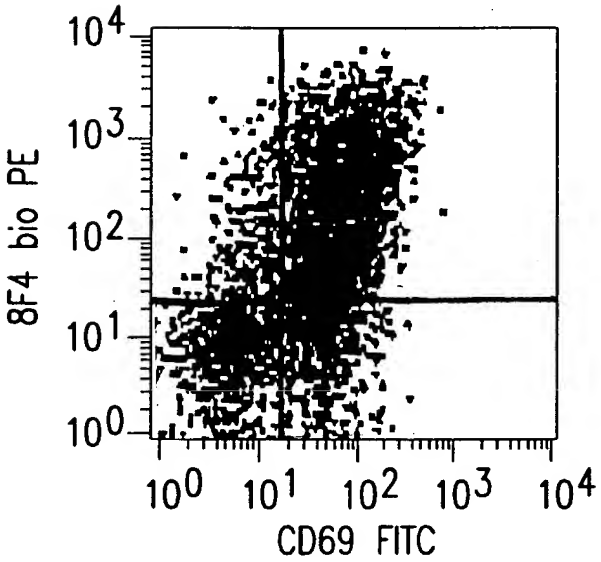

10^4
10^3
10^2
10^1
10^0
8F4 bio PE
10^0
10^1
10^2
10^3
10^4
CD69 FITC

FIG.6B

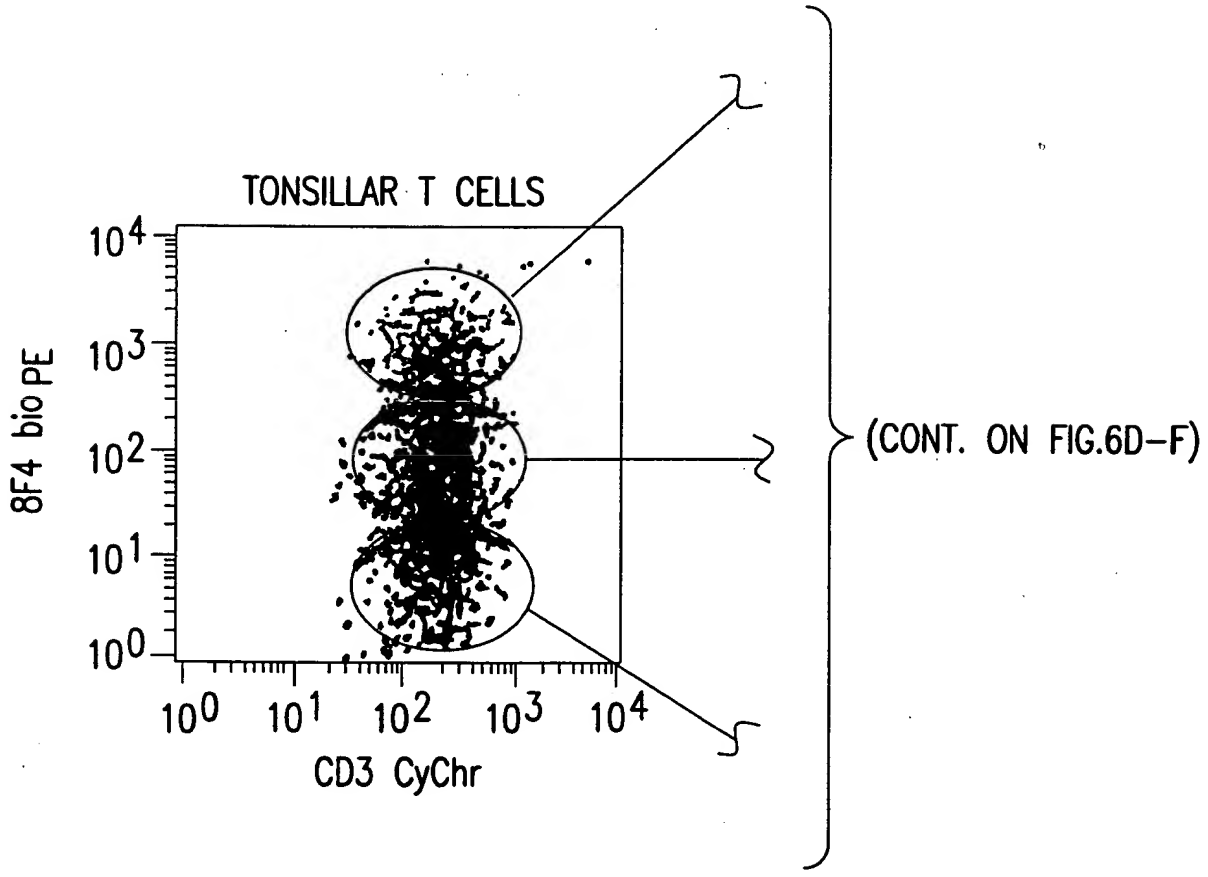
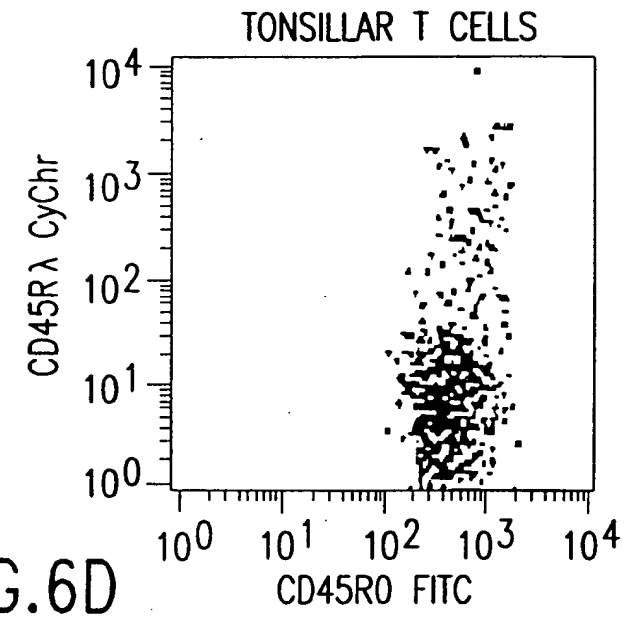

TONSILLAR T CELLS
8F4 bio PE
10^4
10^3
10^2
10^1
10^0
10^0 10^1 10^2 10^3 10^4
CD3 CyChr
(CONT. ON FIG.6D–F)

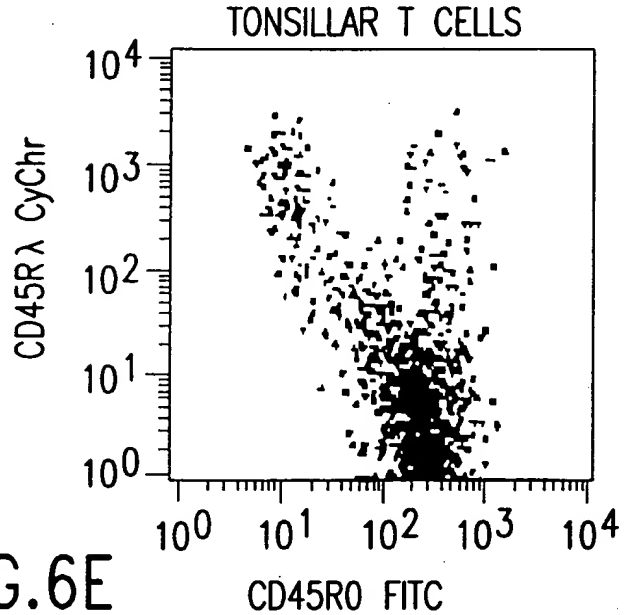
FIG.6C



$8F4^{HIGH}$

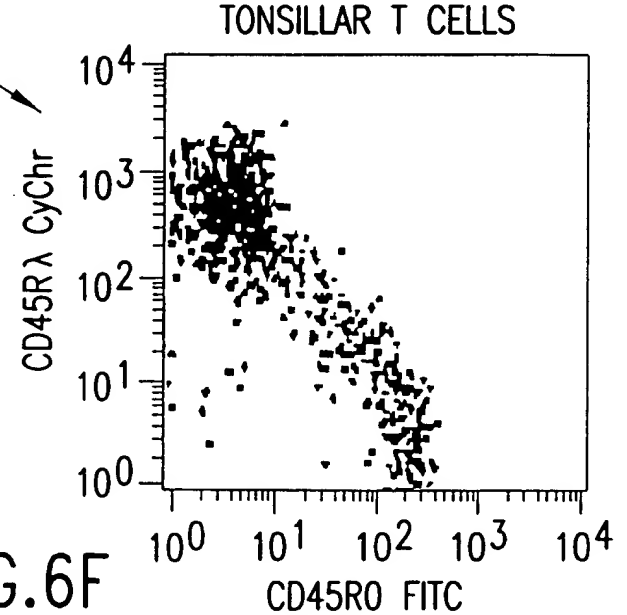
FIG.6D

(CONT. FROM FIG.6C)



$8F4^{LOW}$

FIG.6E



$8F4^{*}$

FIG.6F

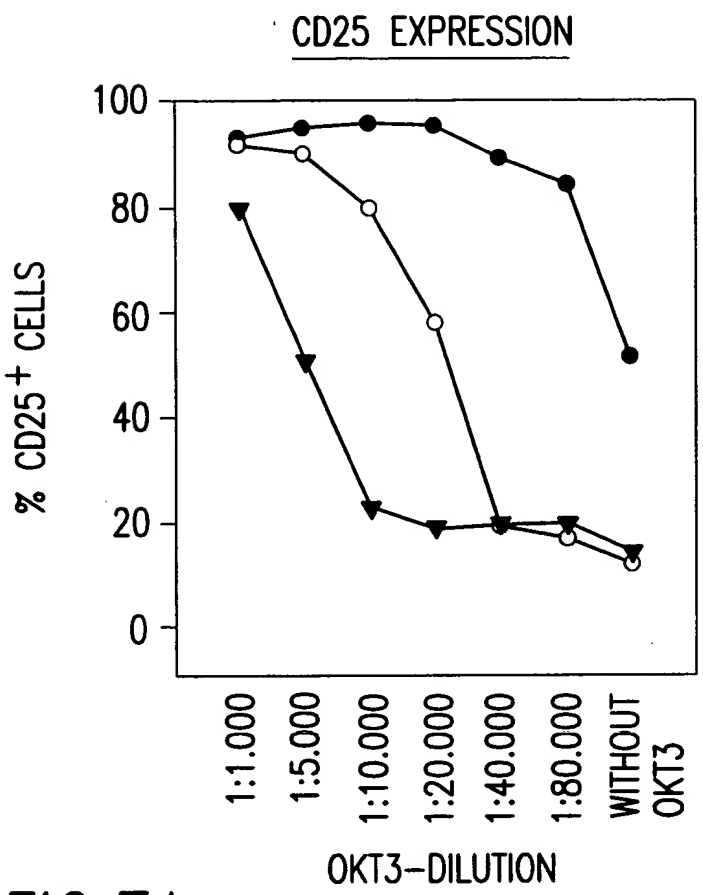

CD25 EXPRESSION
100
80
60
40
20
0
% CD25+ CELLS
1:1.000
1:5.000
1:10.000
1:20.000
1:40.000
1:80.000
WITHOUT OKT3
OKT3-DILUTION

FIG.7A

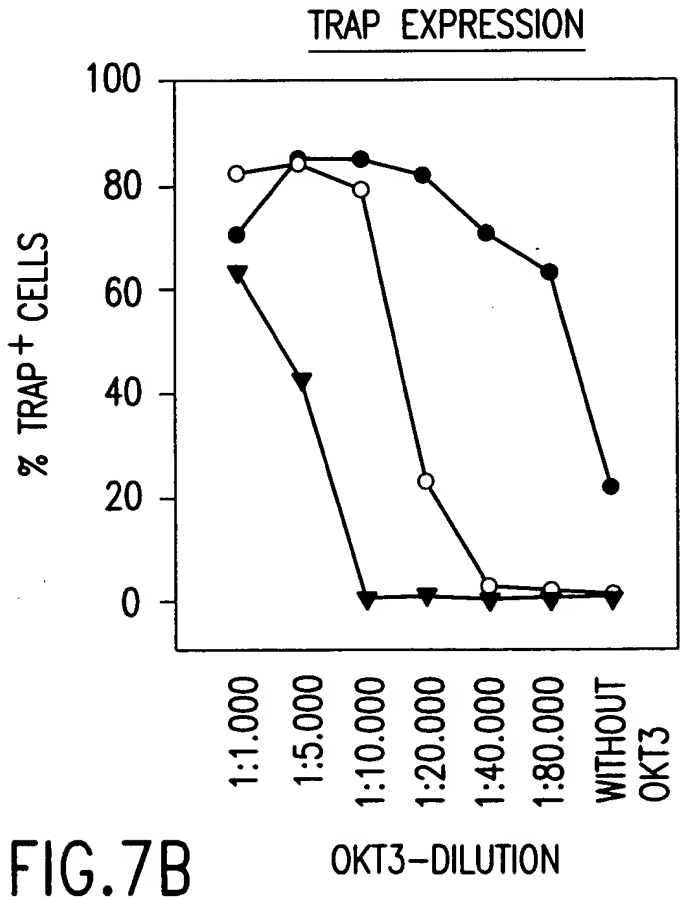

TRAP EXPRESSION
100
80
60
40
20
0
% TRAP+ CELLS
1:1.000
1:5.000
1:10.000
1:20.000
1:40.000
1:80.000
WITHOUT OKT3
OKT3-DILUTION

FIG.7B

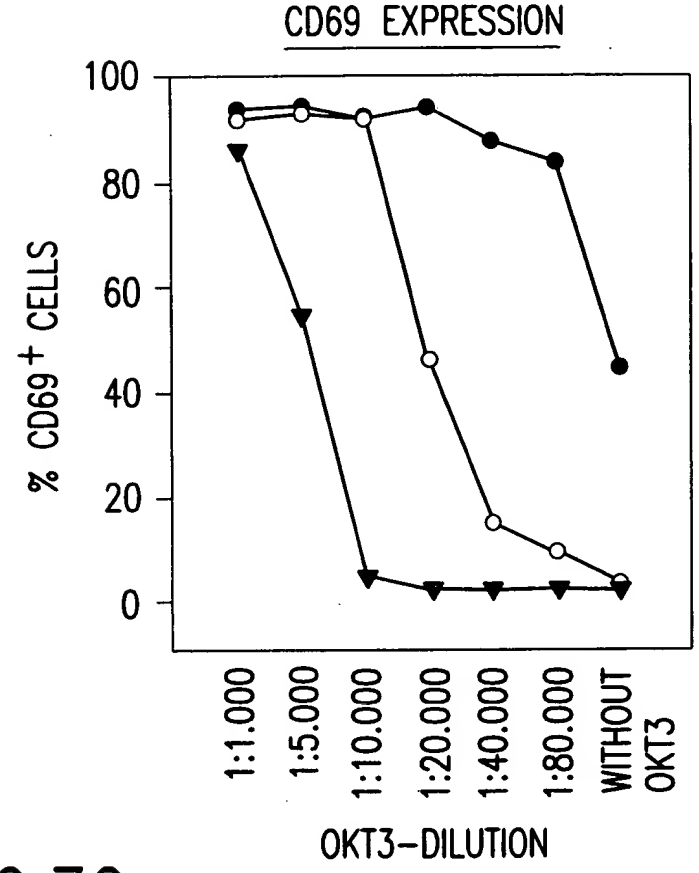

CD69 EXPRESSION
100
80
60
40
20
0
% CD69+ CELLS
1:1.000
1:5.000
1:10.000
1:20.000
1:40.000
1:80.000
WITHOUT OKT3
OKT3-DILUTION

FIG.7C

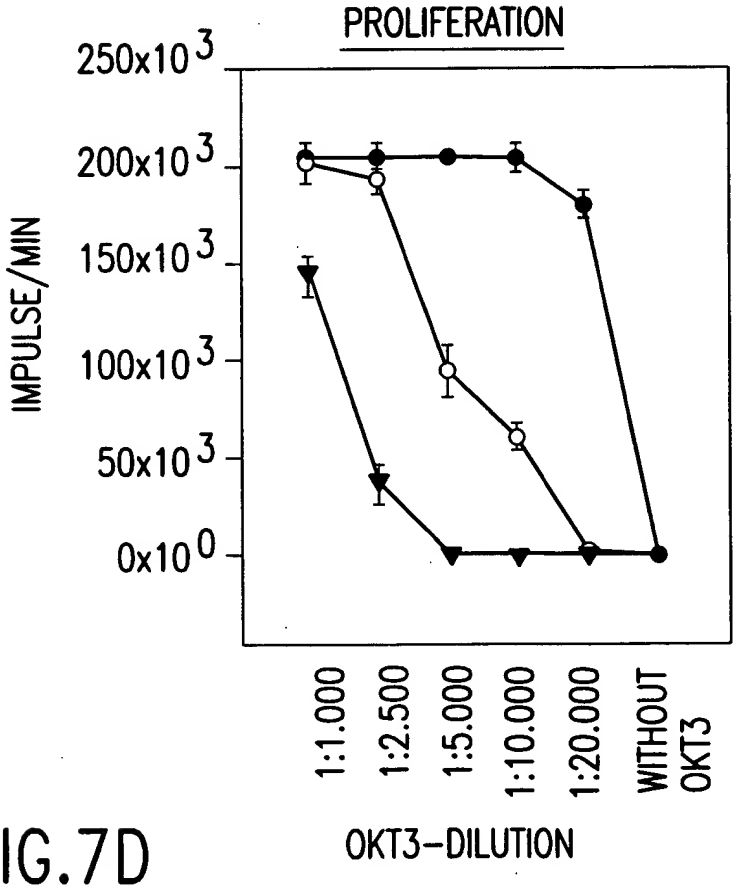

PROLIFERATION
250x10 3
200x10 3
150x10 3
100x10 3
50x10 3
0x10 0
IMPULSE/MIN
1:1.000
1:2.500
1:5.000
1:10.000
1:20.000
WITHOUT OKT3
OKT3-DILUTION

FIG.7D

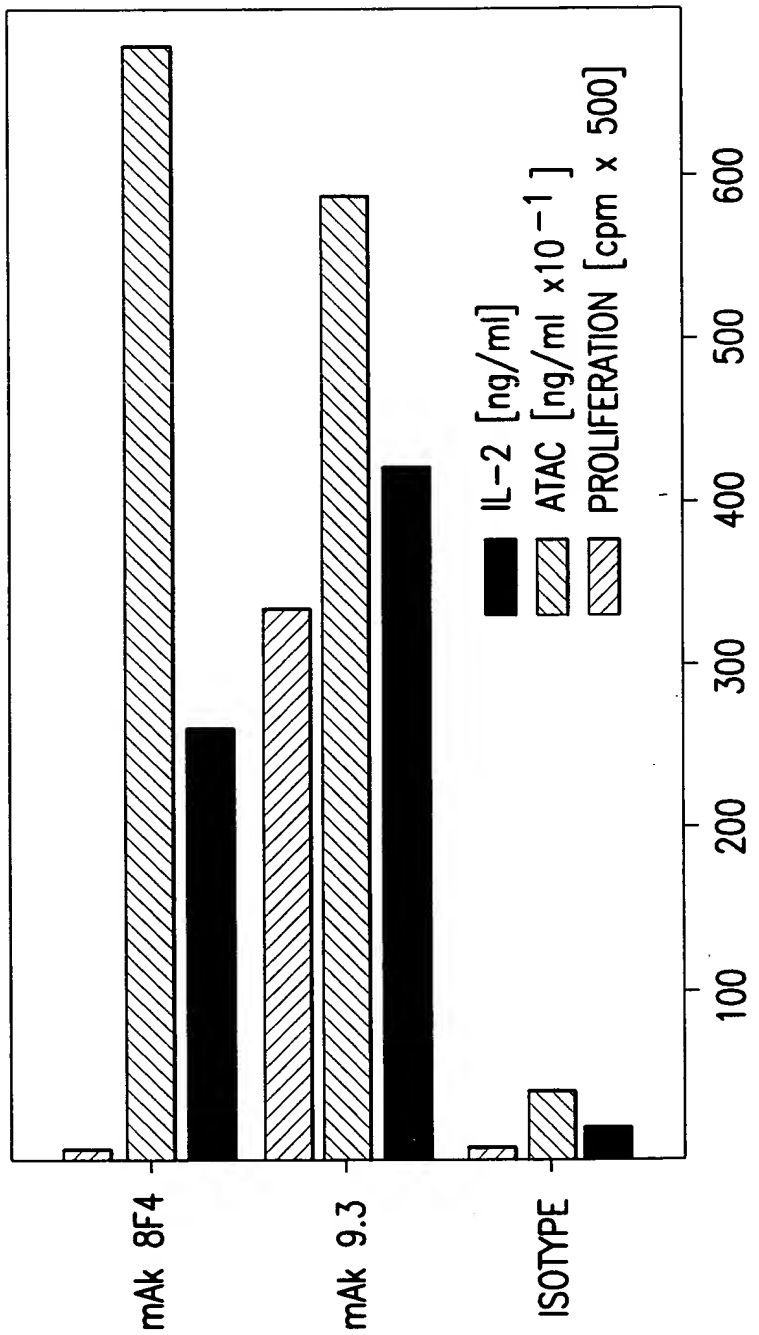

IL-2 [ng/ml]
ATAC [ng/ml x10^{-1}]
PROLIFERATION [cpm x 500]
100
200
300
400
500
600
mAk 8F4
mAk 9.3
ISOTYPE

FIG.8

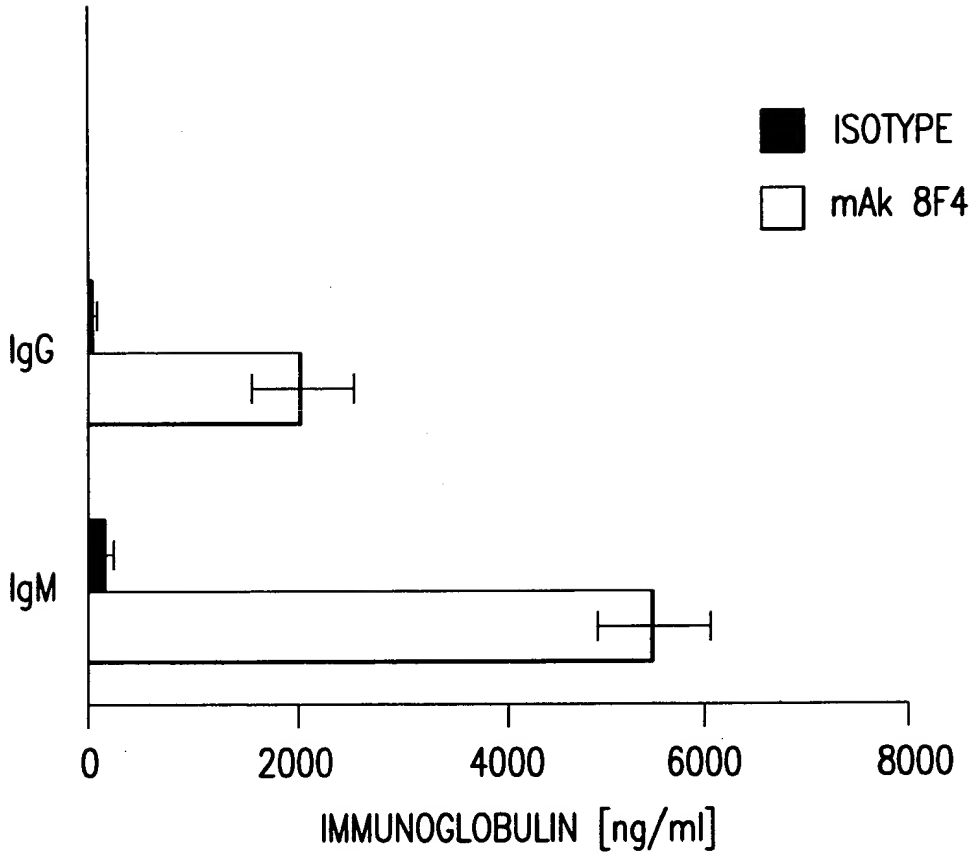

ISOTYPE
mAk 8F4
IgG
IgM
0
2000
4000
6000
8000
IMMUNOGLOBULIN [ng/ml]

FIG.9

DRAFTSMAN

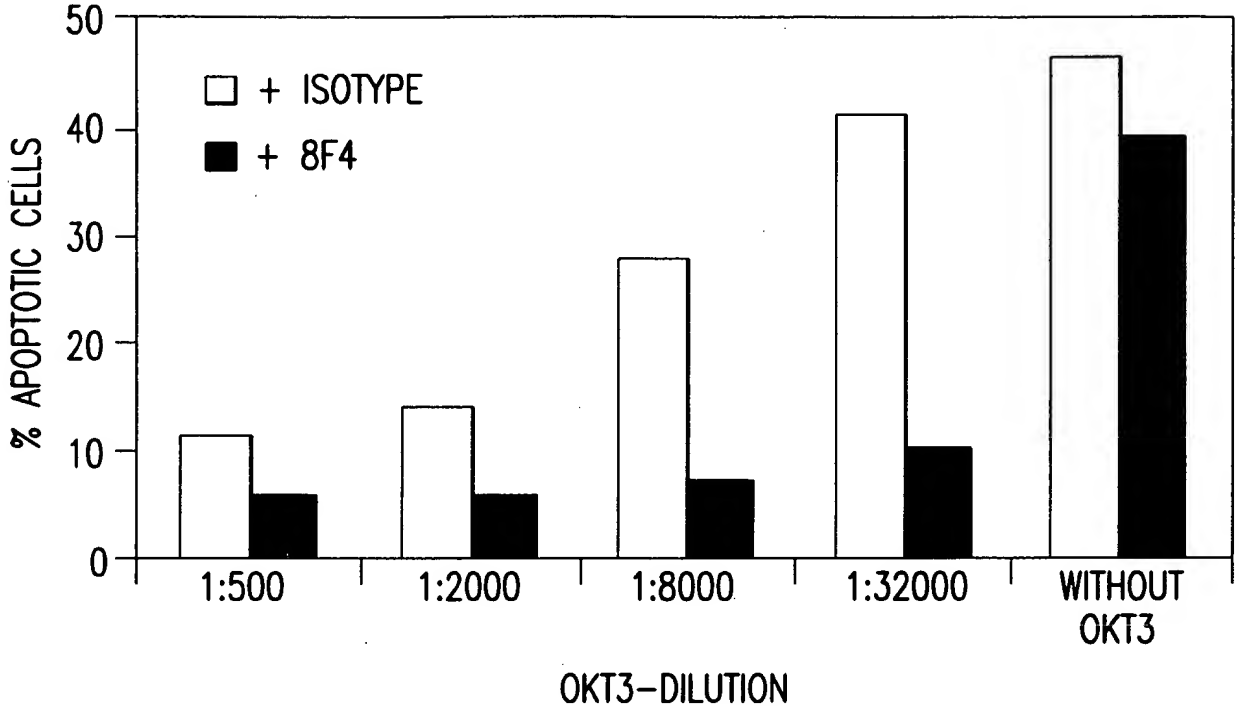


FIG.10

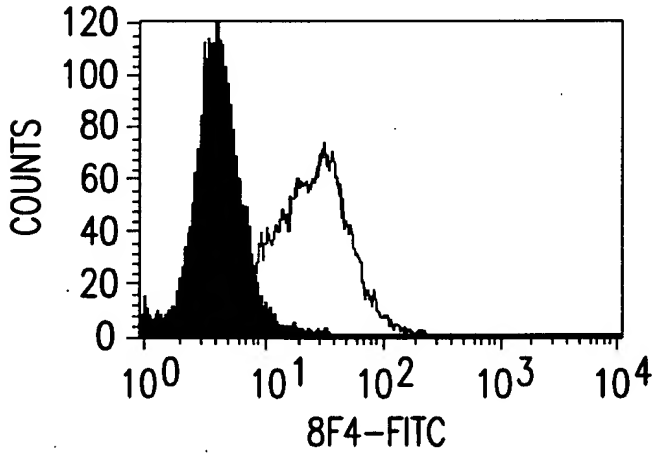


FIG.11

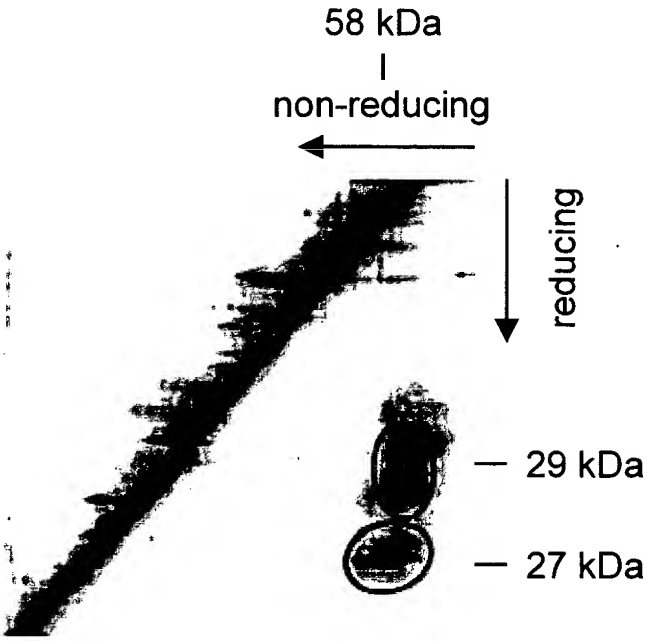


FIG.12

FIG.13

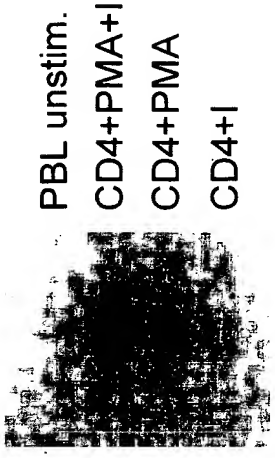


FIG.14A

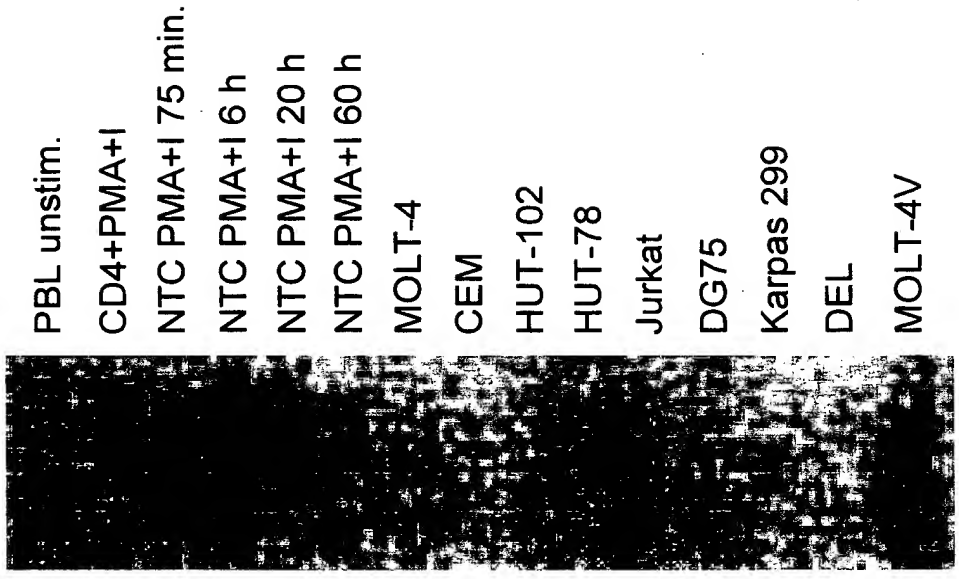


FIG.14B

MKSGLWYFFLFCLRIKVLTGEINGSANYEMFIFHNGGVQILCKYPDIVQQFKMQLLKGGQI
LCDLTKTKGSGNTVSIKSLKFCHSQLSNNSVSFFLYNLDHSHANYYFCNLSIFDPPPFKVT
LTGGYLHIYESQLCCQLKFWLPIGCAAFVVVCILGCILICWLTKKKYSSSVHDPNGEYMFM
RAVNTAKKSRLTDVTL

FIG.15

CGAGAGCCTGAATTCACTGTCAGCTTTGAACACTGAACGCGAGGACTGTTAACTGTTTCT
GGCAAACATGAAGTCAGGCCTCTGGTATTTCTTTCTCTTCTGCTTGCGCATTAAAGTTTT
AACAGGAGAAATCAATGGTTCTGCCAATTATGAGATGTTTATATTTCACAACGGAGGTGT
ACAAATTTTATGCAAATATCCTGACATTGTCCAGCAATTTAAAATGCAGTTGCTGAAAGG
GGGGCAAATACTCTGCGATCTCACTAAGACAAAAGGAAGTGGAAACACAGTGTCCATTAA
GAGTCTGAAATTCTGCCATTCTCAGTTATCCAACAACAGTGTCTCTTTTTTTCTATACAA
CTTGGACCATTCTCATGCCAACTATTACTTCTGCAACCTATCAATTTTTGATCCTCCTCC
TTTTAAAGTAACTCTTACAGGAGGATATTTGCATATTTATGAATCACAACTTTGTTGCCA
GCTGAAGTTCTGGTTACCCATAGGATGTGCAGCCTTTGTTGTAGTCTGCATTTTGGGATG
CATACTTATTTGTTGGCTTACAAAAAAGAAGTATTCATCCAGTGTGCACGACCCTAACGG
TGAATACATGTTCATGAGAGCAGTGAACACAGCCAAAAAATCTAGACTCACAGATGTGAC
CCTATAATATGGAACTCTGGCACCCAGGCATGAAGCACGTTGGCCAGTTTTCCTCAACTT
GAAGTGCAAGATTCTCTTATTTCCGGGACCACGGAGAGTCTGACTTAACTACATACATCT
TCTGCTGGTGTTTTGTTCAATCTGGAAGAATGACTGTATCAGTCAATGGGGATTTTAACA
GACTGCCTTGGTACTGCCGAGTCCTCTCAAAACAAACACCCTCTTGCAACCAGCTTTGGA
GAAAGCCCAGCTCCTGTGTGCTCACTGGGAGTGGAATCCCTGTCTCCACATCTGCTCCTA
GCAGTGCATCAGCCAGTAAAACAAACACATTTACAAGAAAAATGTTTTAAAGATGCCAGG
GGTACTGAATCTGCAAAGCAAATGAGCAGCCAAGGACCAGCATCTGTCCGCATTTCACTA
TCATACTACCTCTTCTTTCTGTAGGGATGAGAATTCCTCTTTTAATCAGTCAAGGGAGAT
GCTTCAAAGCTGGAGCTATTTTATTTCTGAGATGTTGATGTGAACTGTACATTAGTACAT
ACTCAGTACTCTCCTTCAATTGCTGAACCCCAGTTGACCATTTTACCAAGACTTTAGATG
CTTTCTTGTGCCCTCAATTTTCTTTTTAAAAATACTTCTACATGACTGCTTGACAGCCCA
ACAGCCACTCTCAATAGAGAGCTATGTCTTACATTCTTTCCTCTGCTGCTCAATAGTTTT
ATATATCTATGCATACATATATACACACATATGTATATAAAATTCATAATGAATATATTT
GCCTATATTCTCCCTACAAGAATATTTTTGCTCCAGAAAGACATGTTCTTTTCTCAAATT
CAGTTAAAATGGTTTACTTTGTTCAAGTTAGTGGTAGGAAACATTGCCCGGAATTGAAAG
CAAATTTATTTTATTATCCTATTTTCTACCATTATCTATGTTTTCATGGTGCTATTAATT
ACAAGTTTAGTTCTTTTTGTAGATCATATTAAAATTGCAAACAAAATCATCTTTAATGGG
CCAGCATTCTCATGGGGTAGAGCAGAATATTCATTTAGCCTGAAAGCTGCAGTTACTATA
GGTTGCTGTCAGACTATACCCATGGTGCCTCTGGGCTTGACAGGTCAAAATGGTCCCCAT
CAGCCTGGAGCAGCCCTCCAGACCTGGGTGGAATTCCAGGGTTGAGAGACTCCCCTGAGC
CAGAGGCCACTAGGTATTCTTGCTCCCAGAGGCTGAAGTCACCCTGGGAATCACAGTGGT
CTACCTGCATTCATAATTCCAGGATCTGTGAAGAGCACATATGTGTCAGGGCACAATTCC
CTCTCATAAAAACCACACAGCCTGGAAATTGGCCCTGGCCCTTCAAGATAGCCTTCTTTA
GAATATGATTTGGCTAGAAAGATTCTTAAATATGTGGAATATGATTATTCTTAGCTGGAA
TATTTTCTCTACTTCCTGTCTGCATGCCCAAGGCTTCTGAAGCAGCCAATGTCGATGCAA
CAACATTTGTAACTTTAGGTAAACTGGGATTATGTTGTAGTTTAACATTTTGTAACTGTG
TGCTTATAGTTTACAAGTGAGACCCGATATGTCATTATGCATACTTATATTATCTTAAGC
ATGTGTAATGCTGGATGTGTACAGTACAGTACTGAACTTGTAATTTGAATCTAGTATGGT
GTTCTGTTTTCAGCTGACTTGGACAACCTGACTGGCTTTGCACAGGTGTTCCCTGAGTTG
TTTGCAGGTTTCTGTGTGTGGGGTGGGGTATGGGGAGGAGAACCTTCATGGTGGCCCACC
TGGCCTGGTTGTCCAAGCTGTGCCTCGACACATCCTCATCCCCAGCATGGGACACCTCAA
GATGAATAATAATTCACAAAATTTCTGTGAAATCAAATCCAGTTTTAAGAGGAGCCACTT
ATCAAAGAGATTTTAACAGTAGTAAGAAGGCAAAGAATAAACATTTGATATTCAGCAACT
G

FIG.16